

FIGURE 1-1

1 ttcaaaacccgattcccgaggcgccctattgaagatatggggaagttcgacgagatcgatgtcgggtcgagtgtatg 80
 81 gtgatgtgccgttttgggggaggatgagcgagatagccaagactagcattccgttcccacacagagttgggaatttcta 160
 161 ccaaatccaacacttgcgtattggagcgacgatatgggacgcgggaaaaacacatccgttggatcaggagttgtacgatg 240
 241 atctcgagccttatgtgtcgagaatccgagggtatgcttacgtgaactacagggatctcgacatcgggatgaatggagga 320
 321 ggtgaagggtgagaagggtacttatgttgaggctaagggtgtgggggagaagtactttgggtcaactttgatcggtt 400
 401 gggtcgggtgaagacgattgttgatcccaataatgtgttcgaaacgagcagagcattccctcaattccaaactcggttat 480
 481 aaggatcaatgatcaatgagaattttccctttccaaatgtgattacaagttctattgggtcagctttctcaactgctcctat 560
 561 tcatttagattaattcataaacaactattaatttaccagccttttatccggcccggttgccgatttattttcttaagtttt 640
 641 agatgaaatgaaaccgatttagtttttattgagatgagattaacttaatttgcttgaaatttactcacggttgatgtga 720
 721 tatttggaaattaactaaaatgataaaatcggtataaaaataaaatattt^{I1}aaataaaataacataaagaacaata 800
 801 aaataaaataaatttttaattttatttcccttgttttctgtatcatacatctcttcttacttctttaaaggctt 880
 881 ttcaattatcacttaattaataacataagataaaatcgtttaattctataacattaacctaatacacttgcacggtgaacaat 960
 961 caatatgataataataataataataattcaattattaatctacaattttttaattataaagtttatcggtcagtt 1040
 1041 tctgcaagctccgagctccttgtcatcgttagtttctcggtctcaagggtataacgactcggagcgagccctttgct 1120
 1121 tccaatggacgggttgcatcttctgccgtcgttgagctcgattggcggtgcatgctggagtcagagttcctacaaaaaac 1200
 1201 cctaaactagaggtgattaggtgaaattaggtgttggcctgggttccattgtccaaagtttttagtcaacttaaaaaac 1280
 1281 agacttaaatatttatgcttcaaaaatagtttatctgttattatattagcgtgttaattagcttgacaatgggcccgcgag 1360

FIGURE 1-2

1361 gtacggattcgggaccccgatccccgcccatagtgtaatggctcaactgccaagtcagcattggaccgaaattattggac 1440
 1441 acgaagtactaatgtgaaaaaactttacatttgttattttctactttaatactatgctatttttcaaaaatttgaaactttaat 1520
 1521 actatgttttttatatatagtttagtataatcttaatttttatgcaaaattcatctaatgttattgataaaactatttttcgatccgtag 1600
 1601 ctaattatttcgaaggcaagtcaaagtgttattgtggactatgtgagctaataattgaacctttatctctcccaaccactc 1680
 1681 aagttaattgaaccaaactcgatcggttgcggttttcgagctatttcgagccattgttggttatatgcacgtgagatatcaag 1760
 1761 attgacccgaacactttattattatgataaattgtagaaaaaagaaaaacatatattctaagactacatgcataagtgcaaacccct 1840
 1841 gcatgaaagctgctcaacacggtggcatagactcccgccacgtgtccattccacctcatcacctcaccccccacccgttcac 1920
 1921 ctcttattatatcacaacaatcaatcaatcctactcctcactgaaacaaatccgaccaacttatcccaatatttccca 2000
 2001 aacttgattaatttctcagcaat ATG GAT CAG ACG CAC CAG ACA TAC GCC GGA ACC ACG CAG AAC 2065
 1 M D Q T H Q T Y A G T T Q N 14
 2066 CCG AGC TAT GGC GGC GGC ACA ATG TAC CAG CAG CAG CCG AGG TCT TAC CAG GCG 2125
 15 P S Y G G G T M Y Q Q Q P R S Y Q A 34
 2126 GTG AAG GCG GCC ACT GCA GCC ACC GCG GGT GGA TCC CTC ATC GTT CTG TCC GGT CTC ATC 2185
 35 V K A A T A A T A G S L I V L S G L I 54
 2186 CTT ACG GCC ACC GTC ATT TCA CTC ATC ATA GCC ACC CCT CTC CTT GTC ATC TTC AGC CCT 2245
 55 L T A T V I S L I A T P L L V I F S P 74
 2246 GTT CTT GTC CCG GCT CTC ATC ACC GTC GGC CTC TTG ATC ACC GGG TTT CTT GCT TCC GGT 2305
 75 V L V P A L I T V G L L I T G F L A S G 94
 2306 GGG TTC GGA GTC GCC GGC ACC GTC TTG TCC TGG ATC TAT AG gtagtataagctttggactt 2370
 95 G F G V A A V T V L S W I Y R 109
 2371 tagtattgtataaaaatacataagctgatttatgaacatggatctctcccaacaagagttatttaaatgcattctcgggtctg 2450

FIGURE 1-3

2451 actcgatcgggttggttttggagctactcgggtcacaaatggtcggtcggtcggtctggtgatctgttatatactaataatttgggaagcc 2530

2531 tgaagtttcattgttctgcccccaacttcccactaccttttgagggtgtttaagaagccatacaaaaactaatatatgaatccct 2610

2611 cccaacaactcagaacctcgagtcagtgagggttgtgacggttctctatataaacatttcgaaaaatctttgttcaatgaacgtag 2690

2691 aaatgaccatgcttgatgttggttataag G TAC GTG ACC GGC CCG CAC CCG GCG GGA GGG 2756
110 Y V T G G H P A G G 119

2757 GAT TCG CTG GAC CAG GCT AGG TCG AAG CTG GCC GGA AAG GCC AGG GAG GTG AAG GAC AGG 2816
120 D S L D Q A R S K L A G K A R E V K D R 139

2817 GCG TCG GAG TTC GCA CAG CAT GTC ACA GGT GGT CAA CAG ACC TCT TAA agagagtcctct 2879
140 A S E F A Q Q H V T G G Q Q T S * 156

2880 agttaaattggtcttctgttttctgttgcggcgttgtaaaactctcttttaagtgtgctgttttccctttgtctcgtgt 2959

2960 gttgtaagtgaagtgtaatcgaaagtccaagttcgagatgtttgtaacgatgatgttttctaaataatcagagatatataa 3039
3040 aagggttgctaatttagtattgcgtctgatctcggaccaaaactcgcaagtaaaattcgagaggatgagttgttacagaaca Poly A signal 3119

3120 agcgtgcattgttctggaagttcatctccttgagccgacctgtgttgcgttcagtttcgccaaagtccactagacaaatgtt 3199

3200 acgagttaagcctctgtcaaacagatcgctctagcgtcccagaaaaacaccagatttttcgaaaaaccatcggggatcaatt 3279

3280 ttcgattcaaattccgatcttggaaagtacttgaacagaaagcatgatgctaaaaagataataagaaaatcgaaagcctagaaaaag 3359

3360 ttgtacagaaagcaacaagtcaaaaatatagatcaacttcaaaagtttcaaaattacatctttacagaccccccaaaaatgaca 3439

3440 gttaacagaagtgcactaaacagaaaccagcagcttcacctggaatgaaggagcgtttgatcaatccatcctagcttcat 3519

3520 tcccccttgaaaattgcagacagagctctcatctctgctaaagctggtggcttattctttaaccctgcaatcaataagcatga 3599

3600 actaacattggacaccttcatcggcggttgctcgaaaaatcagtgagcggaggtttacctgtgtgtgtagtaacctctc 3679

FIGURE 1-4

3680 tccttgataataatctggaaattccggcatcaactactgccacctttctgcttaagtgattttatcaccaaggctga 3759
3760 gcgtgattccttgcgctcttgctccgaatcctgatgtatccactgagctttccatctccttctccaggccttatgttc 3839
3840 accaatgcgtcctcgccgaacacacactcttggcggtacaaagtgcgagccagggaatccacactctccatcaagtgcagacct 3919
3920 gcaaaccccaataaagaacacaaaactccaaaagtcacgatcaattctccgccttttatgaagaaaaggaaaacttctgggt 3999
4000 acttacggtgccgtcagacacttcataattttagacttgatgatatgtgtccaggaaattccttctcgttctgaattgttgt 4079
4080 gttaacagcaâcctgacagacagaaaagatatcgcaaaatttaagatactgggatgactaggcacagagaaaatgaaatctaa 4159
4160 ttctagaagtaaaaccttattttcccatcacaattctgcccacatagtcgggaacgcagcatccgagcaagaagcaggag 4239
4240 agatgtaatccatgatatcgatgtggatatcggtgaggacgacaaactgaacgttccatcacattgg 4305

1 tctagacatttgacataaaaccgaattcaaaagaacacacaacttgactaacacccccaaaaagaaaatagagttagtgaattttgga 80
R1

81 agattaaaaaatagaaaacaaactgattccttagaaaagaagagatgattagggtgccttcagttcggtctgtgcaggaaaatcga 160
R2

161 gatgttcacttatattacattgtcgattcatctcccaattgtcctgggttcctttactgtgccgacgcgttttttgaatcccag 240
R3

241 ttaattcccatcaagtcttccttcagctgcgtagcactgctagctcctaacaatggagcgtggagtctactcgttcatgggg 320

321 catcgcaaaggttgccttcattgtctgtaccagcgccaccgcctctcttggttgtgtggacaattgcggtgaagc 400

401 gcgcaagttgacatcccatagtctcgacacctcaccatatggatgtttaaaacgtatatcacgagtgcgatctacatgtc 480

481 ccatcacaccacataaaagcaatagtttggagcttttcataatttgaaacgggcattgacgacttgcctctcgataat 560

561 ttaatctttttctcttcagctgattgtgtgcattccgggctcagaagcacatcaaaagggatctctccatcgtagt 640

641 attgggtcgtgtgatgatacgaagcagtcgatgaagtctcctaattgtcgcgagctacaggctccgcaaaagaacccgcga 720

721 ggtagatcgtatgctagtaccccaaaatcagtttgcgtagcgggaatcaacacactagagactcacctaatgcattctcatg 800

801 tgtgatgaacagtttatcatttgtgagcttaggggtcattgtcgtatgacccaatgcacattgagcttatgatagaatttg 880
R3

881 aataggaaagcgttttccaccagatcacgaatagctaccccttttttcgggcgcaaaatttcgggcacatcctatcttccacc 960

961 acaacttaaagatcgcgatcggtaaggaaactcaccgaccacacacatcgaataatcttcggtgaccggttcctgttgatca 1040

1041 agtccctcaatttcctcaacctagtcttcaatgcgcgctagcgttatccccccgcataatggacttttcatagcgcggagcgt 1120

1121 agccggagacgacgagcaagaaggatgagcggcggcagattgcgggctaaagaaacgagcttcctgccttgctctatggag 1200

1201 gcagatttctgagttgatggatttgtgatggtgacacatttttaattaaagttgatttttttagcacttcattcacg 1280

1281 taattaaaataaattccagtatTTTatatatttttcttacgttatctaatttttttgaaagattaaaaactttgatat 1360
R4 R2

FIGURE 2-2

1361	aggcaagatcatgacacgctcgaagttaagtgaatgagactcctaacaaggtaataacaacagcagttcataaacccgaatga	14141	ccttgatctttactaagcttgagatcattgaacatatataattaaatcgtttaatgaaagataagaactttaataataaaaaa	15201	cattcaaaacgagaaactgatacaaaaaaagcaaacgccaacaaaaataatagacggtggaaggatgatgcagagcc	16001	atccaccctttttcccaagtttccttactgcttactctctatgcatatcacaaagacgcccttgaaaacttgttagtcattg	16801	cagagcccttactgcccaggtcacccgacacggtgttactctatcacttctccttctcctttaagaaccaccacgc	17601	cacctccctctcaaaaacactcataaaaaaacccctcttcttgacatttctcccaagttcacaattagttcacagtaagcaag	18401	aactcaacaaca	19031	ATG GCG GAT CGT ACA ACA CAG CCA CAC CAA GTC CAG GTC CAC ACC CAG CAC	19031	M A D R T T Q P H Q V Q V H T Q H	19631	CAC TAT CCC ACC GGC GGC GCT TTC GGC CGT TAT GAA GGT GGA CTC AAA GGC GGT CCA CAT	19631	H Y P T G G A F G R Y E G G L K G G P H	20231	CAC CAG CAA GGA TCA GGC AGC GGC CCA TCA GCT TCC AAG GTG TTA GCA GTC ATG ACC GCG	20231	H Q Q G S G S G P S A S K V L A V M T A	20831	CTC CCC ATC GGC GGC ACC CTC CTT GGC TTG GCC GGG ATA ACC TTG GCT GGG ACG ATG ATC	20831	L P I G G T L L A L A G I T L A G T M I	21431	GGG CTG GCG ATC ACC CCG ATT TTT GTC ATC TGC AGC CCT GTT CTA GTC CCG GCC GCT	21431	G L A I T T P I F V I C S P V L V P A A	22031	CTG CTC ATC GGC TTT GCC GTG AGC GCG TTT CTG GCC TCG GGG ATG GCC GGG CTG ACA GGG	22031	L L I G F A V S A F L A S G M A G L T G	22631	CTG ACC TCG CTG TCG TGG TTT GCG AGG TAT CTG CAG CAG GCT GGG CAG GGA GTT GGA GTG	22631	L T S L S W F A R Y L Q Q A G Q G V G V	23231	GGG GTG CCG GAT AGT TTC GAG CAG GCG AAG AGG CGC ATG CAG GAT GCT GCT GCG TAT ATG	23231	G V P D S F E Q A K R R M Q D A A G Y M
------	---	-------	---	-------	---	-------	--	-------	--	-------	---	-------	--------------	-------	---	-------	-----------------------------------	-------	---	-------	---	-------	---	-------	---	-------	---	-------	---	-------	---	-------	---	-------	---	-------	---	-------	---	-------	---	-------	---	-------	---

FIGURE 2-3

FIGURE 3-1

1 tccactatgtaggtcatatccatcttttaatttttgggaccattccaattccatcttgccctttagggatgtgaatatga 80
5' primer (1) AT rich
81 acggccaaggtaagagataaaaaataatccaaattaaagcaagagaggccaagtaagataaatccaaatgtacacttgtca 160
AT rich
161 tcgccgaaattagtaaaatcgcgcatattgtattcccacacattattataaaataccgtatatgtattggtgcatttgc 240
241 atgaataatactacgtgtgaagcccaaaagaccacgtgtagcccatgcaaaagttaaacactcacgacccccattccctcagt 320
RY G box seed-specific
321 ctccactatataaaacccaccatcccccaatcttaccaaaacccaccacacgactcacaaactcgactctcacacaccttaaaaga 400
TATA 3' primer (1)
401 ccaatcaccacccaaaaaATGGAAAGCTGATGAGCCTAGCAGCCGTAGCAACGCGAGTTCCCTCTTCTGATCGTGGTGAC 480
1 M A K L M S L A A V A T Q F L F L I V V D 21
481 GCATCCGTCCGAACACACAGTGATTATCGACGAGGAGACCAACCAAGCCGGGTGGAGGCAAGGTGGCAGGGACAGCAGC 560
22 A S V R T T V I I D E E T N Q G R G G K V A G T A A 48
561 AGTCTGCGAGCAGATCCAGCAGCGAGACTTCCTGAGGAGCTGCCAGCAGTTTCATGTGGGAGAAAGTCCAGAGGGCG 640
49 V C E Q Q I Q Q R D F L R S C Q Q F M W E K V Q R G G 75
641 GCCACAGCCACTATTACAACCAAGGCGGTGGAGGAGGCGAAGAGCCAGTACTTCGAACAGCTGTTGTGACGACCTTA 720
76 H S H Y Y N Q G R G G G E Q S Q Y F E Q L F V T T L 101
721 AGCAATTGGCACCGCGGTGCACCATGCCAGGGGACTTGAAGCGTGCCATCGGCCAAATGAGGCAGGAAATCCAGCAGCA 800
102 S N C A P R C T M P G D L K R A I G Q Q M R Q E I Q Q Q 128
801 GGGACAGCAGCGGACAGCAGGAAAGTTCAGAGGTGGATCCAGCAAGCTAACAAATCGCTAAGGACCTCCCCGGAC 880
129 G Q Q Q Q Q Q E V Q R W I Q Q A K Q I A K D L P G Q 155

[illegible]

FIGURE 4-1

10 20 30 40 50 60 70 80 90 100
 ctcaagcatacggacaagggttaataacataagtcaccagacaataataacaaaaagtcagaagcaagataaaaaaattagctatggacattcaggttc
 110 120 130 140 150 160 170 180 190 200
 atattggaaacatcattatccttagtctgtgaccatccttctcctcctgctctagttagaggcccttgaggactaacgagaggtcagttgggtagcagatcc
 210 220 230 240 250 260 270 280 290 300
 ttatcctggactagccttctggtgttcagagtccttcgtgcccgcgtctacatctatctccatttaggtctgaagatgactcttcacaccaacgacgtttt
 310 320 330 340 350 360 370 380 390 400
 aaggtctctactactcctagcttgcaatacctggcttgcaatacctggagcatcgtgcacgatgattggatactgtggaggaggaggtgtttgctgatt
 410 420 430 440 450 460 470 480 490 500
 tagagctcccgttggtgatttgacttcgatttcagtttaggctgttgaaattttcaggtccattgtgaagccttttagagcttgagcttcccttcca
 510 520 530 540 550 560 570 580 590 600
 tgттаatgccttgatcgaaattctctctagagaaaaagggaagtcgatctctgagtatgaaatcgaaagtcacattttttttcaacgtgtccaatcaatcca
 610 620 630 640 650 660 670 680 690 700
 caaacaagcagaagacaggtaattctcactatactactgacaagtaatagcttaccgtcatgcataataacgtctcgttcccttcaagagggttttc
 710 720 730 740 750 760 770 780 790 800
 cgacatccataacgacccgaagcctcatgaaagcattagggaagaacttttggttcttctgtcatggccttttatagggttcagccgagctcgccaattc
 810 820 830 840 850 860 870 880 890 900
 ccgtccgactggctccgcaaaatattcgaacggcaagttatggacttgcaaccataactccacgggtattgagcaggacacctattgtgaagactcatctcat
 910 920 930 940 950 960 970 980 990 1000
 ggagcttcagaatgtggtgtcagcaaaccaatgaccgaaatccatcacatgacggacgtccagtggtgagcgaaacgaaacaggaagcgccctatctt
 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100
 cagagctgtgagctccacacccggttcggcaactacgtgttggtggcaggttcgcgtattagagatatgttgaggcaagaccatctgtgccactcgta
 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
 caattacgagaggtgtttttttgtgatttttccctaagtttctcgttggtgagctcatattctacatcgatggtctctcaacgtcgtttcctgtcat

FIGURE 4-2

1210 1220 1230 1240 1250 1260 1270 1280 1290 1300
 ctgatatcccgctcatttgcatccacgtgcccgcctcccggtgcaagtccttagtgatgacgcccgaattggtggtggtgcggtgcccctgtgctt
 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400
 cttaaccgatgggtgaggttgagtttgggggtctccgcggcgatggtagtgggttgacgggttgggtgacggcattgatcaaatcttactcttgc
 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500
 ttcaaatctttggcagaaaaacaattcattagattagaaactggaaaccagagtgatgagacggattaaagtcagattccaacagagttacatctcttaaga
 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600
 aataatgtaacccctttagacttttatattttgcaattataaaataatttaacttttagacttttatatatagttttaataactaaagttaaccactcta
 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700
 ttatttatatcgaaactattttgtatgtctccctctaaataaaacttggtattgtgtttacagaacctataatcaataataactcaactgaagtgtg
 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800
 tgcagttaattgaagggttaacgcccgaatgcactagattatcaaccgaatagattcacactagatggccatttccatcaatatcatcgccgttctt
 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900
 cttctgtccacatatccctctgaaacttgagagacacctgcacttcattgtccttattacgtgttaaaaaatgaaacccatgcatccatgcaaaactgaa
 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000
 gaatggcgcaagaacccttccctccatttcttatgtggcgaccatccatttccaccatctcccgctataaaacaccccccatcacttcacctagaaacatca
 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100
 tcactactgttattccatccaaaagatacccaccATGGTAGATCATCAAGCCCTTGTCTCTCACTCTGCAATTTTGGCCATTCTCTCCACTCTTC
 2110 2120 2130 2140 2150 2160 2170 2180 2190 2200
 TCTGGGTAGCAGCAATTCCAGCAGGGGAACGAGTGCAGATCGACAGGATCCGAGCGGACAAAACCATCCAGGAGAGAGCTGGCACCATC
 L G R Q Q F Q Q G N E C Q I D R I D A S E P D K T I Q A E A G T I
 2210 2220 2230 2240 2250 2260 2270 2280 2290 2300
 GAGGTATGGGACCAGAACCCGACGCAATTCAGTGGCTGGTGTGGCGTTGTAAGCGGCACCATTTAGCCCAAGGTCTTCTTGCCTTTCTACAGCA
 E V W D Q N R Q Q F Q C A G V A V V R R T I E P K G L L L P F Y S

ABRE
 R1
 R2
 CAAT
 TATA
 Legumin Vicilin
 Signal sequence
 M A R S S S P L L L S L C I F A I L F H S S

FIGURE 4-3

2310 2320 2330 2340 2350 2360 2370 2380 2390 2400
ACACCCCTCAGCTCATCTACATCGTTCAAGgtataaaatcagttcatacaatgataaccaccacttcgaatgtatttatcaaatatcaatgatcga
N T P Q L I Y I V Q

2410 2420 2430 2440 2450 2460 2470 2480 2490 2500
tgcacctgtatgtgtgtatattcagTAGGGGAGTTACAGGAATCATGTCCCAKATGTCCAGAGACATTCCAGGAATCCAGCAGCAAGGACAAC
G R G V T G I M F P X C P E T F E S Q Q Q G Q

2510 2520 2530 2540 2550 2560 2570 2580 2590 2600
AGGGCCACAGGGTAGTTCCCAAGACAGCACACCAGAAAGATCCGCCGCTTCGTGAAGGTGACGTCAATTGCCGTCCCTGCCGTGTAGCCCACTGGTCCTA
Q G Q Q G S S Q D Q H Q K I R F R E G D V I A V P A G V A H W S Y

2610 2620 2630 2640 2650 2660 2670 2680 2690 2700
CAACGATGGCAACGAACCAAGTCATGGCCATTGTTGCCATGACACTTCCAGCCACCTCAACCAACTGGACAACAACCCAGGgtatataagcattgccgt
N D G N E P V M A I V V H D T S S H L N Q L D N N P R

2710 2720 2730 2740 2750 2760 2770 2780 2790 2800
agttgctaataaattgcacacaattggaactctatttcagtatctaataacttttcccttttttgccagAACTTCTACTTGGCAGGAAACCCGAGAGAC
N F Y L A G N P R D

2810 2820 2830 2840 2850 2860 2870 2880 2890 2900
GAGTTCGAACAATCGCAGCAAGGAGCGAGGTAGCCCTGGGGAGAGTGAAGTGGACGAGGACCGAGGGAACCTCTTCAACCTGCAACAACCTCTTCTT
E F E Q S Q Q G G R L S R G E S E G G R G R E P L Q P A T T S S

2910 2920 2930 2940 2950 2960 2970 2980 2990 3000
GCGGAATCGACTCCAAGTCAATCGGGAGGCGTTCAATGTGACGAGAACCTGGCAAGGAGGTACAGAGCGGAGAACGACAACAGAGGCCAGATCGTCCG
C G I D S K L I A E A F N V D E N V A R R L Q S E N D N R G Q I V R

3010 3020 3030 3040 3050 3060 3070 3080 3090 3100
AGTCGAAGCGAGCTCGACATCGTCAGACCTCCGACCAAGTATCCAGAGGAGTCCAGGAGGACGAGGAGGTCTGTGGTGGTGGCCGCTACTACTCCAATGGA
V E G E L D I V R P P T S I Q E E S Q E Q G G R G G G Y Y S N G

3110 3120 3130 3140 3150 3160 3170 3180 3190 3200
GTGGAGGAGACCTTCTGCTCCATGAGACTAATTGAGAACATCGCGCATCTTCTCGGGCAGACATTTTCACTCCAGAGCGGCGCGGTAGATCCCTCA
V E E T F C S M R L I E N I G D P S R A D I F T P E A G R V R S L

FIGURE 4-4

3210 3220 3230 3240 3250 3260 3270 3280 3290 3300
ACAGCCACAACCTCCCGTCTGCAATGGATCCAGCTTAGCGCCGAGAGAGCGGTTCTCTACAATgtatagatctcactcacgcaccaactctctaaattga
N S H N L P V L Q W I Q L S A E R G V L Y N
3310 3320 3330 3340 3350 3360 3370 3380 3390 3400
atccctaattatttaattcaccgatctctgaccgacccggtttgtagGAAGCGATCAGGCTGCCGACTGGAACATCAACGCACACAGCATAGT
E A I R L P H W N I N A H S I V
3410 3420 3430 3440 3450 3460 3470 3480 3490 3500
GTACCGGATCAGAGGACACAGCAGATCCAGATCGTGAACGAGGAGGAATTCGGTGTTCGATGGAGTGTGCAGGAAGGACAGGTGGTGACGGTGCCG
Y A I R G Q A R V Q I V N E E G N S V F D G V L Q E G Q V V T V P
3510 3520 3530 3540 3550 3560 3570 3580 3590 3600
CAGAACTTCGCGGTGGTAAAGAGATCCCAGAGCGAGAGGTTTGAGTGGTGGCGTTCAAGACCAACGACAAACGCGATGGTGAACTCGCTAGCCGGGAGGA
Q N F A V V K R S Q S E R F E W V A F K T N D N A M V N S L A G R
3610 3620 3630 3640 3650 3660 3670 3680 3690 3700
CATCGGCAGTAAGGGCGATCCCGCGGATGTACTGGCTAACGCCCTGAGGGGTGTCGCCGGAGGAGCGGAGGAGGTGAAGTTCAACAGGAGGAGACTCA
T S A V R A I P A D V L A N A W R V S P E E A R R V K F N R Q E T H
3710 3720 3730 3740 3750 3760 3770 3780 3790 3800
CTTGGCTAGCACAGGGCCAGTCCAGGTCCCGCGGAGGTTGAATCGTCAAGGAGGTGATCAACTTGCTTATGTAAaatgtgacggtgaaataataa
L A S T R G Q S R S P G R L N V V K E V I N L L M *
3810 3820 3830 3840 3850 3860 3870 3880 3890 3900
cggtaaaatatatgtaataataataaagccacaaagtgagaatgaggggaagggaaatgtgtaatgagccagtagccggtgtgtgtaattttg
3910 3920 3930 3940 3950 3960 3970 3980 3990 4000
tatcgtattgtcaataaatcatgaattttgtgttttttaaatcatgaatttttaaaattttataaaataatctccaatcggaagaacaac
4010 4020 4030 4040 4050 4060 4070 4080 4090 4100
attccatatccatggatgtttcttttaccacaaatctagtctttgagaggatgaagcatcacccaagcttctgcaaatatccctcaaaagcttttaaaatga
4110 4120 4130 4140 4150 4160 4170 4180 4190 4200
acaacaaggaaacagagcaacggtccaaagatcccaaacgaaacatatattatctataactataattattataattactactgtcccggaatcacaaatccct

FIGURE 4-5

4210 4220 4230 4240 4250 4260 4270 4280 4290 4300
gaatgattcctattaactacaagccttgttgccgagagaagtgtatcgccgagcagaagcagcagcactcgagacgagccttgatgagcagagtc
4310 4320 4330 4340 4350 4360 4370 4380 4390 4400
tttacctgcagggcggtgaaggggaagagcgcccttctggagtaggagttcagcaagcggcggttccttggcggagtaagcggacgtaaggggtggtgtgc
4410 4420 4430 4440 4450 4460 4470 4480 4490 4500
gacgtcntcgttcnggagcggnattcatgaagggttaagtcanaatctgtagctctcgagtgcagggagccnaaagacgttgggaaacccgtcgcncgt
4510 4520 4530 4540 4550 4560 4570 4580 4590 4600
ttggggcatcagtcngcggggcacgccttcctcctgctcctccanaancnangtanatttaaaaganatgggaaattaantaatggnnaatnannagagg
4610 4620 4630 4640 4650 4660 4670 4680 4690 4700
attgnaacggtcnganccgnanganaagttttannnggttaataactggggagtgngnagccngcncctggtccngttagangaaacccaagnnccgg
4710 4720 4730 4740 4750 4760 4770 4780 4790 4800
gaggnnttcannngnaggagaaaaaggannncatttnannangcngagggacatgaancggtaacngagctgnggttcannnancggcgnnngnagtcc
4810 4820 4830 4840 4850 4860 4870 4880 4890 4900
cnnnggaccnggtggggtanaaagggaanggaacattnggtngnangganaanaaccnttttaacnattgccttgcaggnngtntnggcncntncgggt
4910 4920 4930 4940 4950 4960 4970 4980 4990
nacatncgcgtgcacatgggcttggggngccnanagnagccncanggggnannngcnccttgtnccangcgcctnaagttcnattgtanatggncggttg

FIGURE 5

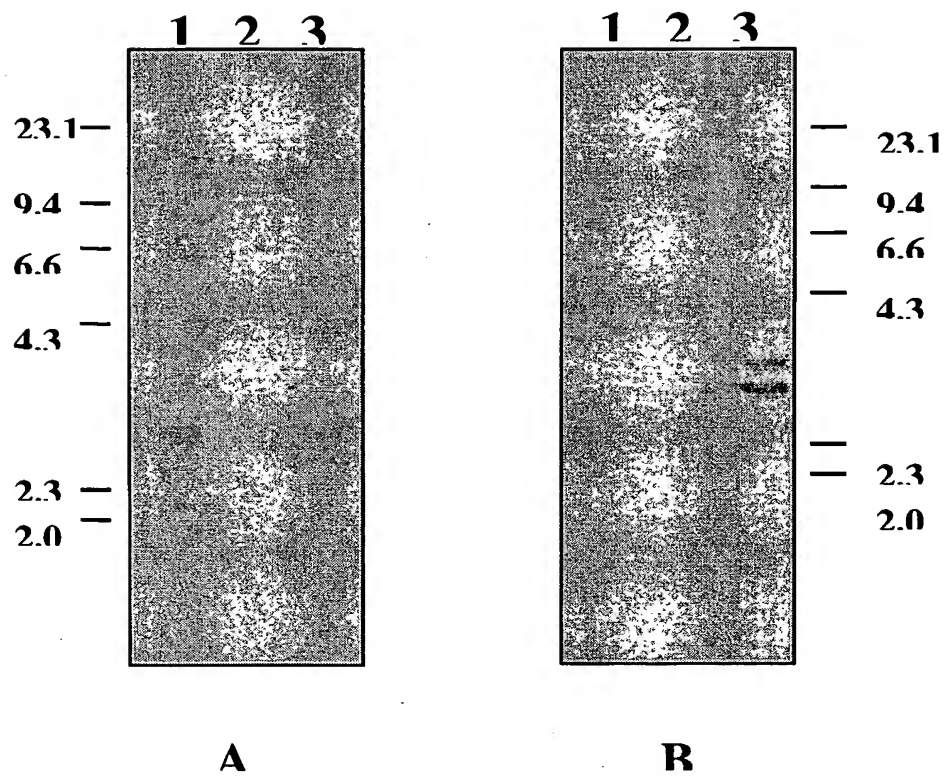


FIGURE 6

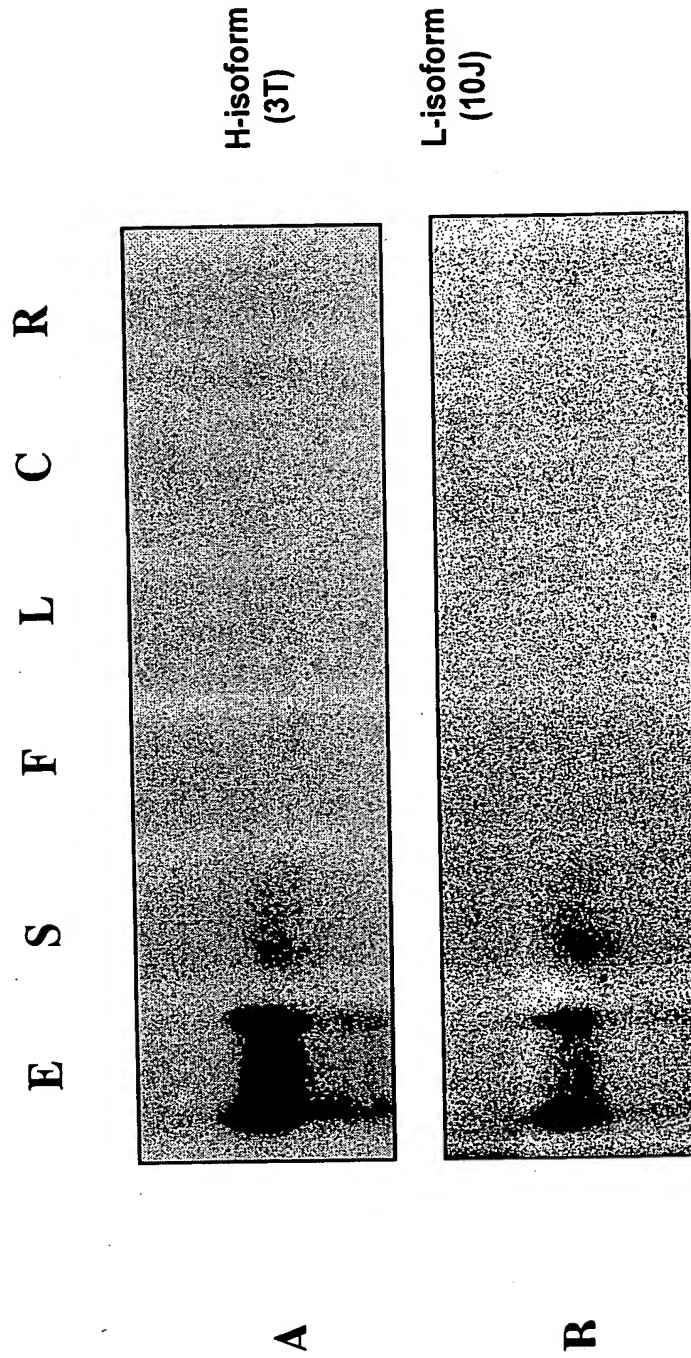


FIGURE 7

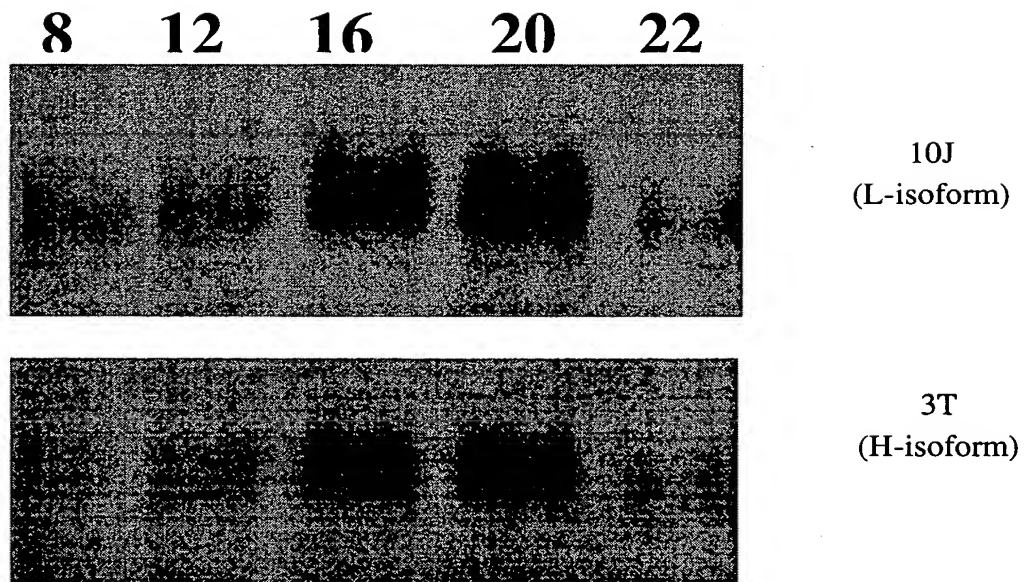


FIGURE 8

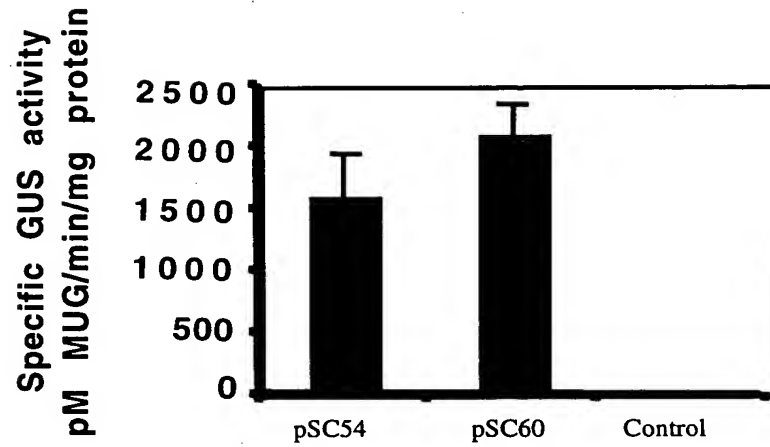


Figure 9.1

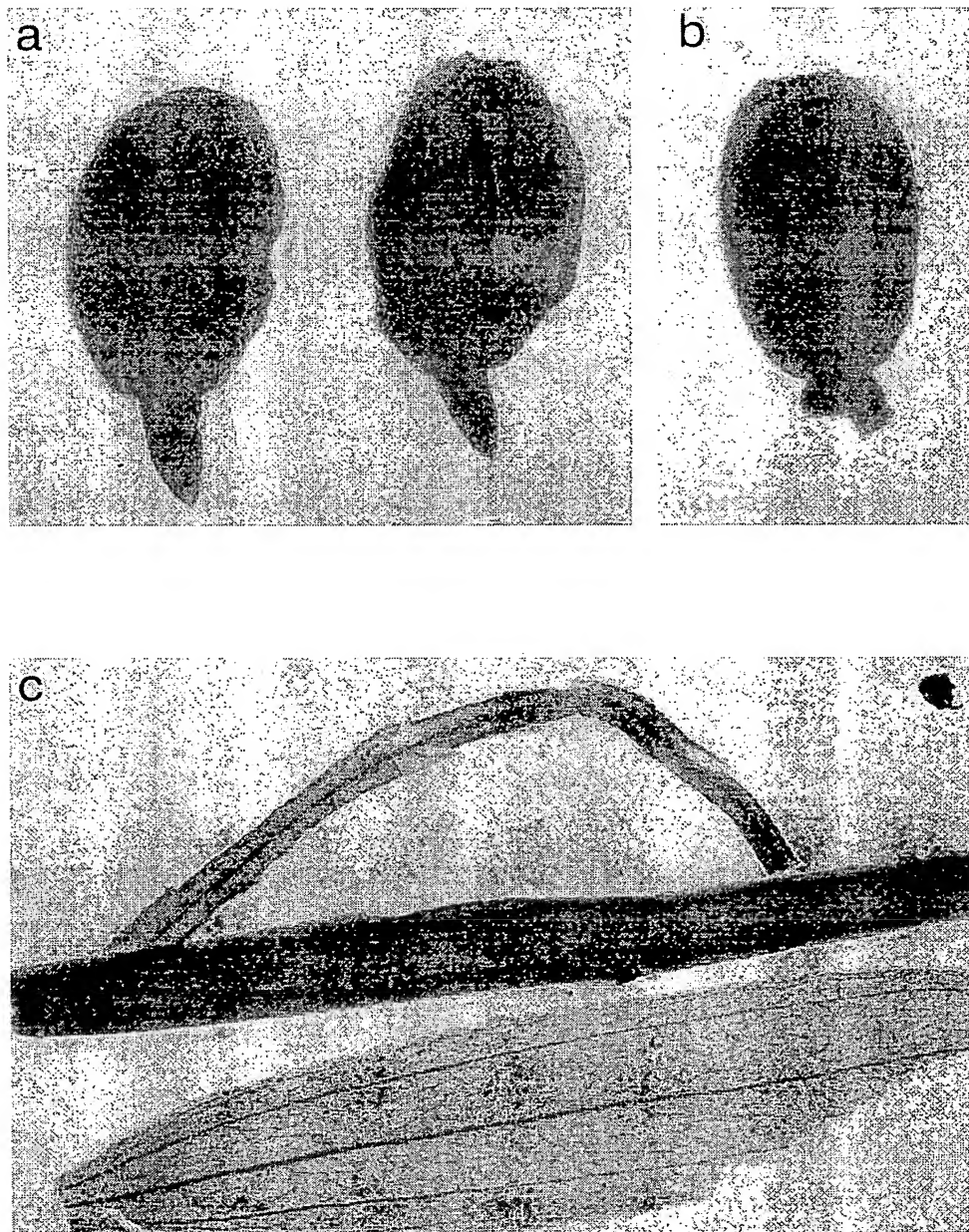


Figure 9.2



FIGURE 10

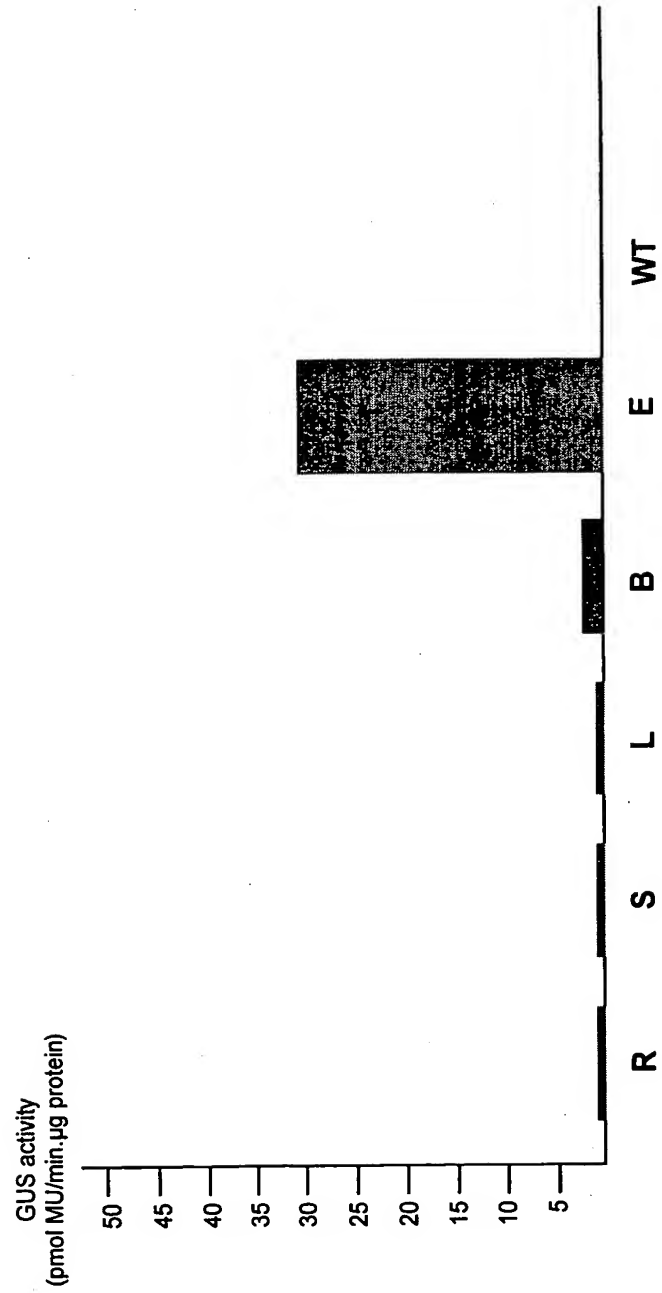


FIGURE 11

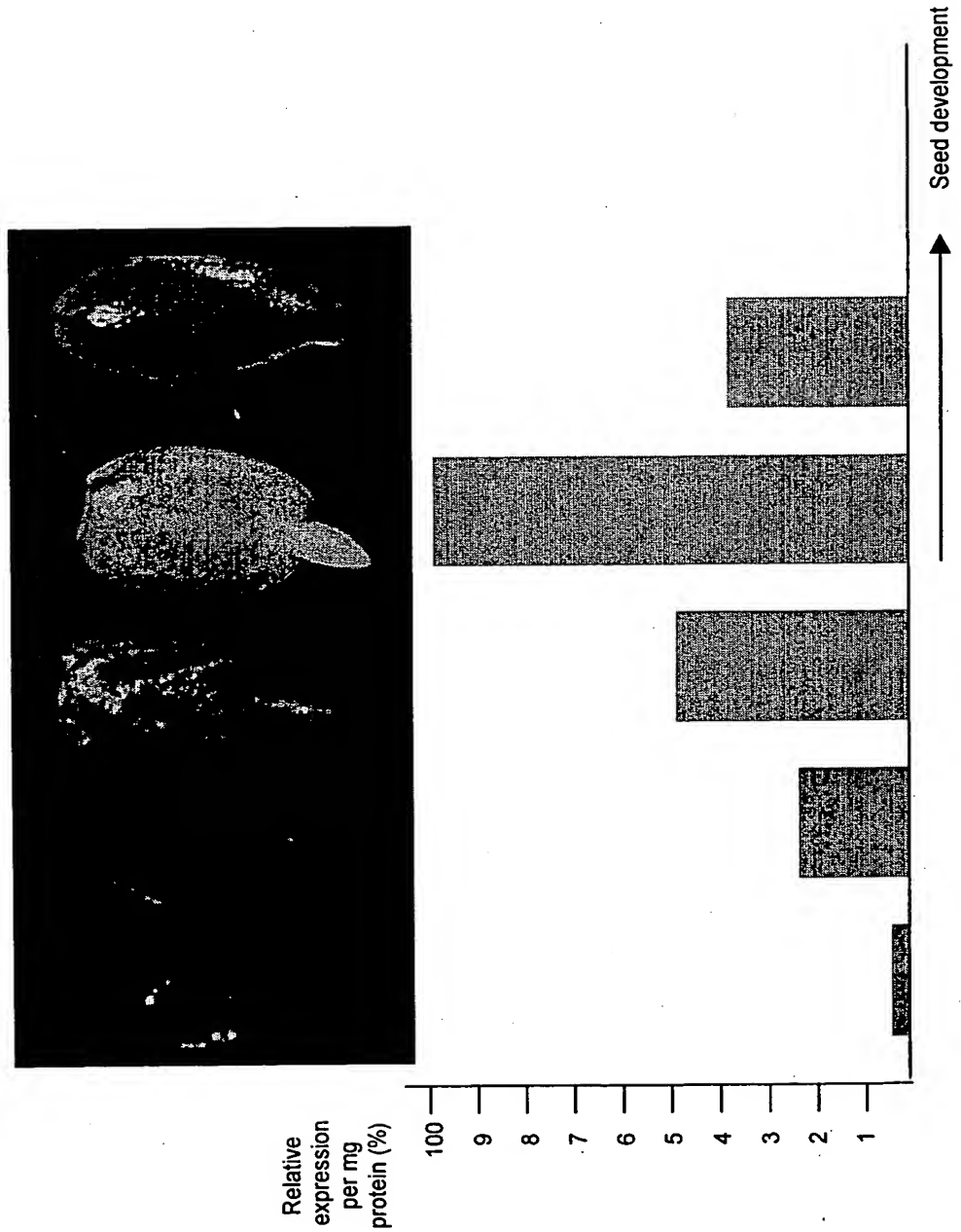


FIGURE 12

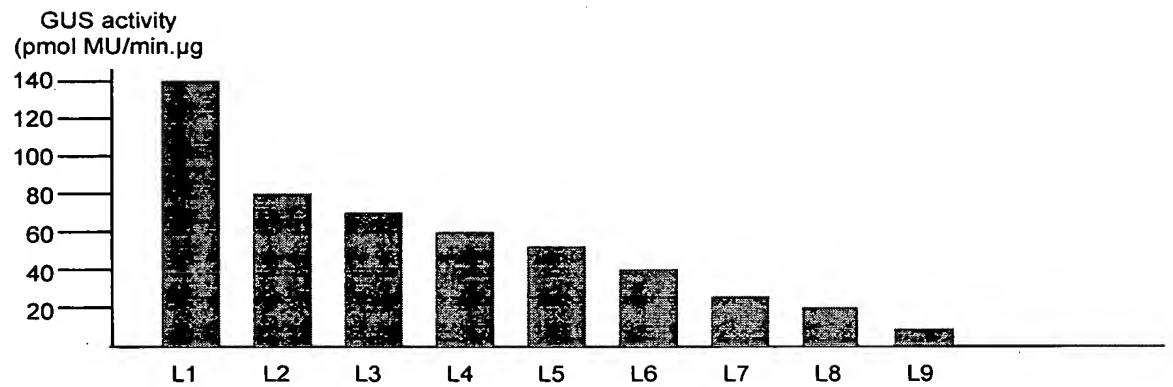


FIGURE 13

